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EXAMINER

KAPUSHOC, STEPHEN THOMAS

ART UNIT	PAPER NUMBER
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1634

DATE MAILED: 09/11/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/805,973	ZHAO ET AL.	
	Examiner	Art Unit	
	Stephen Kapushoc	1634	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☒ Responsive to communication(s) filed on 16 June 2006.
- 2a) ☒ This action is **FINAL**. 2b) ☐ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 1-9, 14-24 and 29-31 is/are pending in the application.
- 4a) Of the above claim(s) _____ is/are withdrawn from consideration.
- 5) ☐ Claim(s) _____ is/are allowed.
- 6) ☒ Claim(s) 1-5, 7, 8, 14-19, 21-23 and 29-31 is/are rejected.
- 7) ☒ Claim(s) 6, 9, 20 and 24 is/are objected to.
- 8) ☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☒ The drawing(s) filed on 16 June 2006 is/are: a) ☒ accepted or b) ☐ objected to by the Examiner.
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some * c) ☐ None of:
1. ☐ Certified copies of the priority documents have been received.
 2. ☐ Certified copies of the priority documents have been received in Application No. _____.
 3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).
- * See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

- | | |
|--|---|
| 1) <input type="checkbox"/> Notice of References Cited (PTO-892) | 4) <input type="checkbox"/> Interview Summary (PTO-413) |
| 2) <input type="checkbox"/> Notice of Draftsperson's Patent Drawing Review (PTO-948) | Paper No(s)/Mail Date. _____ |
| 3) <input checked="" type="checkbox"/> Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) | 5) <input type="checkbox"/> Notice of Informal Patent Application (PTO-152) |
| Paper No(s)/Mail Date <u>6/16/2006</u> . | 6) <input type="checkbox"/> Other: _____ |

DETAILED ACTION

Claims 1-9, 14-24 and 29-31 are pending.

Claims 10-13, 25-28, and 32-41 are cancelled.

This Office Action is in reply to applicants' correspondence of 06/16/2006. Claims 10-13, 25-28, and 32-41 have been cancelled; no claims have been newly added. Applicants' remarks and amendments have been fully considered but are not found to be persuasive. Any new grounds of rejection presented in this Office Action are necessitated by Applicants' amendments. Any rejections or objections not reiterated herein have been withdrawn. This Action is made FINAL.

Claim Rejections - 35 USC § 103

1. The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

(a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negated by the manner in which the invention was made.

2. Claims 1, 7, 8, 14, 15, 21-23, and 29 are rejected under 35 U.S.C. 103(a) as being unpatentable over Hucl et al (2003) (WO 03/014357) in view of DelRio-LaFreniere et al (2001).

Hucl et al teaches the molecular basis of imidazolinone resistance in wheat plants. The reference teaches that resistance to imidazolinone can be conferred by a guanine to adenine substitution in the AHASL1 gene (referred to in Hucl et al as Asl1), which results in a serine to asparagine substitution (p.7 Ins. 1-15; Figure 8 page 17/42; p.13 Ins 2-3; Figure 13). Hucl teaches the nucleic acid and deduced amino acid sequences of the AHSAL1 genes of several imidazolinone resistant wheat plants (Fig 8)

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including the mutation responsible for herbicide resistance. The reference teaches that imidazolinone resistant mutant alleles can be detected by amplifying AHASL1 genes and comparing the amplified gene sequence to that of a known wild-type control (p.17 ln.33-p.18 ln.13; p.20 ln.26-p.21 ln.2). Relevant to step (a) of claim 1, the reference teaches the use of genomic DNA (p.18 ln.11). Relevant to step (b) of claim 1, Hucl et al teaches the portion of the AHASL1 nucleic acid sequence that is responsible for the imidazolinone resistance-mutation, including nucleotides 3-23 of SEQ ID NO: 12 of the instant application (for example see Fig 8, p17/42 of the figures, (SEQ ID NO: 15) the nucleotides encoding the amino acid sequence HVLPMP(N/S) beginning at amino acid 620).

Regarding claim 7, Hucl et al teaches the AHASL1 nucleic acid sequence that includes the sequence relevant to SEQ ID NO: 3 of the instant application (for example see Fig 8, p14/42 of the figures, row 4 (SEQ ID NO: 15) the nucleotides encoding amino acids GEAlIA, beginning at amino acid 451).

Regarding claim 8, Hucl teaches that there are AHAS genes on genomes A, B, and D of the *Triticum* wheat plant (p.9 lns. 25-33), and teaches the sequence of the *Imi1* wheat gene (Fig 8; p.7 lns.1-15), which is the AHASL1D gene on the D genome, as evidenced by Pozniak et al (2004) (p.1439 – Chromosome location of AHAS genes).

Regarding claims 15, 21, and 23, the teachings of Hucl et al and DelRio-LaFreniere et al are applied to steps (a), (b), and (d) of claim 15 as they were applied to claims 1, 7 and 8 earlier in this rejection. Additionally, Relevant to step (c) of claim 15, Hucl et al teaches the wild-type AHASL1 nucleic acid sequence that is responsible for

imidazolinone sensitivity, including the sequence relevant to SEQ ID NO: 10 of the instant application (for example see Fig 8, p17/42 of the figures, (SEQ ID NO: 21) nucleotides that encode amino acids 621-633, HVLPMIPSGGAFKD).

Regarding claim 21, Hucl et al teaches the AHASL1 nucleic acid sequence that includes the sequence relevant to SEQ ID NO: 3 of the instant application (for example see Fig 8, p14/42 of the figures, row 4 (SEQ ID NO: 15) the nucleotides encoding amino acids GEAlIA beginning at amino acid 451).

Regarding claim 22, Hucl teaches the AHASL1 nucleic acid sequence that includes the sequence relevant to SEQ ID NO: 4 of the instant application (for example see Fig 8, p17/42 of the figures, row 4 (SEQ ID NO: 15) nucleotides that encode amino acids 621-627, VLPMIP(N/S)).

Regarding claim 23, Hucl teaches that there are AHAS genes on genomes A, B, and D of the *Triticum* wheat plant (p.9 Ins. 25-33), and teaches the sequence of the *Imi1* wheat gene (Fig 8; p.7 Ins.1-15), which is the AHASL1D gene on the D genome, as evidenced by Pozniak et al (2004) (p.1439 – Chromosome location of AHAS genes).

Hucl does not teach the analysis of AHASL1 genes via allele specific PCR using oligonucleotide primers, or primers with mismatches as are required for primers directed to nucleotides 3 to 23 of SEQ ID NO: 12 wherein the 3'-end nucleotide is cytidine (step (b) of claims 1 and 15, step (c) of claim 30).

DelRio-LaFreniere et al teaches a method for the detection of single nucleotide polymorphisms using allele-specific primers that contain additional intentional mismatches (p.201 – Methods and results; p.202, right col., last paragraph). Relevant

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to step (b) of claim 1, the reference teaches a PCR reaction comprised of genomic DNA from whole blood (p.203- DNA purification), dNTPs, a polymerase, forward and reverse gene specific primers (referred to in the reference as LS1 and LS2 (locus specific) primers), and a mutant-allele-specific primer (referred to in the reference as AS-MUT) (p.204-PCR setup conditions). The reference teaches that mutant and wild-type allele specific primers are designed to flank the polymorphic position (p.203 – Prothrombin mutation (factor II), FVL), and that additional mismatches within the primers can increase amplification specificity by making primers refractory to amplification of non-cognate alleles; the reference further indicates that the ideal nature (e.g. pyrimidine to pyrimidine or purine to purine) and locations (e.g. antepenultimate, penultimate) of mismatches can be experimentally determined (p.202, right col., ln.46 – p.203, left col., ln.9; Table 3; p.207, left col., lns.4-10). Relevant to step (c) of claim 1, DelRio-LaFreniere et al teaches the detection of PCR products using gel electrophoresis and ethidium bromide staining (p.204, right col., lns.8-11). DelRio-LaFreniere et al teaches that the allele specific primer is capable of annealing to a region of the analyzed gene that is nested between the annealing sites of the gene-specific primers (Fig. 1).

Regarding claims 14 and 29, DelRio-LaFreniere et al teaches the detection of PCR products using gel electrophoresis and ethidium bromide staining (p.204, right col., lns.8-11; Figs. 2, 4).

Relevant to step (c) of claim 15, DelRio-LaFreniere also teaches the use of wild-type allele-specific-primers for detection of wild-type alleles (Tables 1 and 3; Figure 1; p.202, right col., lns.15-18).

Therefore it would have been *prima facie* obvious to one of skill in the art at the time the invention was made to have modified the mutation detection methods of Hucl et al so as to have used the allele-specific amplification and primers designed with intentional mismatches primers of DelRio-LaFreniere et al. One would have been motivated to do so because of the teaching of DelRio-LaFreniere et al that indicate intentionally mismatched allele-specific amplification methods provide accurate results (p.205, right col., Ins.22-31) and are simple to perform (p.201 – Methods and results), and further teaches that various intentional mismatches can be tested for optimum specificity (p.203, left col., Ins.9-14; Table 3; p.207, left col., Ins.16-25).

The combined methods would have necessarily included experimentation, as suggested by DelRio-LaFreniere et al (p.207, let col., Ins.4-25), to select primers for mutation detection. Such experimentation would thus include creating the claimed oligonucleotides such as SEQ ID NOs: 3 and 4, and mutant-allele-specific primer nucleotide sequences that have cytidine at the 3' end and wild-type-allele-specific primer nucleotide sequences that have guanosine at the 3', or any other primers which contain 3' end and/or internal mismatches with regard to their cognate binding sites. It is noteworthy that claims that do not recite specific SEQ ID NOs of primers encompass a variety of primers; for example, the mutant-allele-specific primer of claim 1 step (b) requires that 'the 3'-end nucleotide of said nucleotide sequence is cytidine'. The claim does not require that the cytidine is at the 3' terminus, thus one may consider any primer with a cytidine at a position other than the 5' terminus as satisfying this claim limitation. Further, regarding the specific primers and binding sites listed in the claims,

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the selection of any primers within the sequence taught by Hucl et al, following the guidance given by DelRio-LaFreniere et al would have been prima facie obvious to one of skill in the art. One would have expected any primer from within this sequence to function within the methods taught by Hucl et al in view of DelRio-LaFreniere et al for the detection of the mutation taught by Hucl et al. Absent a secondary consideration, such as an unexpected result, the claimed invention is prima facie obvious.

3. Claims 2, 4, 5, 16, 18, 19, and 30 are rejected under 35 U.S.C. 103(a) as being unpatentable over Hucl et al (2003) (WO 03/014357) in view of DelRio-LaFreniere et al (2001) and further in view of Stanton (2002) US Patent 6,475,736.

The teachings of Hucl et al in view of DelRio-LaFreniere et al are applied to claims 2, 4, 5, 16, 18, 19, and 30 as they were previously applied to claims 1, 7, 8, 14, 15, 21-23, and 29 earlier in this office action.

Hucl et al in view of DelRio-LaFreniere et al teaches a method for the detection of mutant AHASL alleles that confer tolerance to imidazolinone on a wheat plant. The method utilizes allele-specific primers with intentional mismatches for amplification, and uses mutant and wild-type specific primers.

Hucl et al in view of DelRio-LaFreniere et al does not teach a pre-amplification step using primers that amplify a product that contains nested annealing sites for the gene-specific primers used to detect specific mutations.

Stanton teaches methods for the analysis of DNA using amplification of polymorphic sites. Relevant to claims 2, 16, and 30 step (b), Stanton teaches that the

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PCR amplification step of a genotyping procedure can be modified to increase sensitivity by using nested PCR (two rounds of PCR, first with an outside set of primers, then with an inside set) (col.34 Ins.35-39).

Regarding claims 4 and 18, Hucl teaches that there are AHAS genes on genomes A, B, and D of the *Triticum* wheat plant (p.9 Ins. 25-33), and provides an alignment of the three different imidazolinone resistance genes (Fig. 12). The sequences taught by Hucl et al include primer binding sites for which it would be a necessary property that oligonucleotide primers directed to those regions would anneal to AHASL1a, AHASL1B, and AHASL1D.

Regarding claims 5 and 19, which depend from claims 2 and 16 respectively, Hucl teaches the AHASL1 sequence that includes the sequence relevant to SEQ ID NO: 1 of the instant application (for example see Fig 12, p39/42 of the figures, nucleotides 901-920).

Therefore it would have been prima facie obvious at the time the invention was made to have modified the mutation detection methods of Hucl et al in view of DelRio-LaFreniere et al so as to have incorporated a pre-amplification step as taught by Stanton. One would have been motivated to do so based on the teachings of Stanton that a pre-amplification step can increase the sensitivity of the methods (col 34 Ins.36-37). One would have had a reasonable expectation of success because Stanton teaches the pre-amplification step in association with PCR based methods, and the allele detection methods of DelRio-LaFreniere et al are PCR based. Further regarding claims 5 and 19, it would be obvious to use primers comprising the claimed sequence

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(SEQ ID NO: 1) given the alignment of the three imidazolinone resistance genes (Fig. 12 of Hucl et al) and the consensus sequence that indicates this region is conserved among the three genes, as use of such a primer would allow for subsequent analysis of any of the three AHASL1 genes from any of the three wheat genomes.

4. Claims 3, 17, and 31 are rejected under 35 U.S.C. 103(a) as being unpatentable over Hucl et al (2003) (WO 03/014357) in view of DelRio-LaFreniere et al (2001) and Stanton (2002) US Patent 6,475,736 and further in view of Werle et al (1994).

The teachings of Hucl et al in view of DelRio-LaFreniere et al and Stanton are applied to claims 3, 17, and 31 as they were previously applied to claims 2, 16, and 30 earlier in this office action.

Hucl et al in view of DelRio-LaFreniere et al and Stanton teaches a method for the detection of mutant AHASL alleles that confer tolerance to imidazolinone on a wheat plant. The method utilizes a pre-amplification step, followed by the use of allele-specific primers with intentional mismatches for amplification, and uses mutant and wild-type specific primers.

Hucl et al in view of DelRio-LaFreniere et al and Stanton does not teach the use of an exonuclease following the pre-amplification step.

Werle et al teaches the use of exonuclease I to degrade excess primers and nucleotides from PCR products prior to analysis by sequencing. Relevant to claims 3, 17, and 31, Werle et al teaches pre-amplification of a PCR product from genomic DNA,

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followed by treatment with exonuclease, then analysis of the exonuclease treated PCR product using the same conditions as for PCR of genomic DNA (p.4354, Ins.20-36).

Therefore it would have been prima facie obvious at the time the invention was made to have modified the mutation detection methods of Hucl et al in view of DelRio-LaFreniere et al and Stanton so as to have incorporated an exonuclease digestion step as taught by Werle et al. One would have been motivated to do so based on the teachings of Werle et al that exonuclease digestion removes factors that interfere with analyses that utilize PCR based methods (p.4354 ln.13-16; p.4354 ln.34-37), and that the exonuclease method is simple to use with minimum sample handling, risk of cross-contamination and amount of DNA template required, and the method is reliable, convenient, and cost effective (p.4355 Ins.1-6). One would have had a reasonable expectation of success because Werle asserts that the method has broad applicability in mutational analysis by a PCR based method (p.4355 Ins.6-8), and the allele-specific amplification method of DelRio-LaFreniere et al is a PCR based method.

Conclusion - Claim Objections

5. Claims 6, 9, 20, and 24 are objected to as being dependent upon a rejected base claim, but would be allowable if rewritten in independent form including all of the limitations of the base claim and any intervening claims.

6. Claims 6 and 20 require SEQ ID NO: 2, and claims 9 and 24 require SEQ ID NO: 7. The sequence of the 3' end (the portion of the gene downstream from the G→A (Ser→Asn) mutation site at position 1594 of the AHASL1D gene in Figure 4 of the

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instant application) of the AHASL1D gene from wheat was known in the prior art of GenBank entry BJ296872 (2002). The sequence of GenBank entry BJ296872 contains the binding sites for SEQ ID NO: 2 (the AHASL common reverse primer) and SEQ ID NO: 7 (the AHASL1D gene-specific reverse primer) as well as the mutation site and the sequence relevant to SEQ ID NOs 3 and 4 (the mutant- and wild-type -allele-specific primers, respectively). However, the sequence in GenBank entry BJ296872 is identified only as a wheat expressed sequence tag (EST) from a cDNA library of mRNA 3'-ends. The sequence is not identified as being a portion of the AHASL1D gene, and there is no teaching in the GenBank entry for one of skill in the art to use the sequence to design primers for the detection of a mutant allele that confers imidazolinone resistance. Additionally, while the prior art of Hucl et al teaches that there are multiple wheat genomes (A, B, and D), each of which contains an AHAS gene of a particular sequence (p.9 lns.23-33), the reference does not provide any particular motivation to use sequence additional to that provided in Figure 8 of Hucl et al for the design of primers for the detection of a mutant allele that confers imidazolinone resistance.

Response to Remarks

Amendments to the Drawings

The newly filed Drawings are acceptable. The previous objections to the drawings are withdrawn.

Sequence compliance

The amendments to the sequence listing to include the nucleic acid and amino acid sequences of Figures 1, 3, and 4 have been considered. The Application complies with the Sequence Compliance rules.

Objection to the Specification

In light of the newly submitted sequence listing, the objection to the specification regarding Fig 1C is withdrawn.

Objections to the Drawings

In light of the newly submitted drawings and sequence listing, the objections to the drawings are withdrawn.

Objections to the Claims

The Objections to claims 6, 9, 20, and 24 are maintained for the reasons set forth in the Office Action of 03/16/2006 and reiterated in this Office Action. The objection to claims 4 and 18 as indicated on the Office Action Summary of 03/16/2006 has been withdrawn.

The rejection of Claims under 103(a)

Applicants have traversed the rejection of claims 1-5, 7-8, 14-19, 21-23, and 29-31 as obvious over Hucl et al in view of DelRio-LaFreniere et al. Applicants argue that the method of Applicants' claimed invention involves the use of a mutant-allele-specific

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primer that has a cytidine as the 3'-end nucleotide and that is capable of annealing to the complement of nucleotides 3 to 23 of SEQ ID NO: 12 (p. 16 of arguments). The arguments further assert that such methods are disclosed in the instant specification on pages 7, 17, and 18, and that such methods are unexpected in view of the prior art teachings regarding primers with intentional mismatches (p.16 of arguments). This argument has been fully considered but is not found to be persuasive.

The rejected claims are broadly drawn to methods comprising amplification using a mutant-allele-specific primer described (claims 1-5, 8, 14-19, 22-23, and 29-31) as:

'comprising a nucleotide sequence with a 5' end and a 3' end, wherein said nucleotide sequence is capable of annealing to the complement of nucleotides 3 to 23 of SEQ ID NO: 12 and wherein the 3'-end nucleotide of said nucleotide sequence is cytidine'

The breadth of the claimed mutant-allele-specific primer is noted. The only structural requirement set forth by the claims is that the '3'-end nucleotide of said nucleotide sequence is cytidine'. However, because the claims are drawn to a primer 'comprising' (and thus primer may contain any amount of any additional sequence) a sequence capable of annealing to the complement of nucleotides 3 to 23 of SEQ ID NO: 12, the claims do not clearly set forth the particular nucleotide sequence of the claimed mutant-allele-specific primer. The claims thus do not require a mutant-allele-specific primer consisting of a nucleotide sequence complementary to nucleotides 3 to 23 of SEQ ID NO: 12 wherein the 3'-terminal nucleotide is a cytidine. Additionally, while the claims require that the mutant-allele-specific primer is 'capable of annealing to' particular nucleotides of SEQ ID NO: 12; the claims do not set forth any particular requirements for the condition of hybridization, thus adding to the breadth of the possible primer

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sequences satisfying the limitations of the claim. Claims 7 and 21 further limit claims 1 and 15 with the requirement that:

‘said mutant-allele-specific primer comprises the nucleotide sequence set forth in SEQ ID NO: 3’

Thus, because claims 7 and 21 are drawn to a primer ‘comprising’ (and thus the primer may contain any amount of any additional sequence) the nucleotide sequence set forth in SEQ ID NO: 3, the claims do not clearly set forth the particular nucleotide sequence of the claimed mutant-allele-specific primer.

The specification teaches only the allele-specific amplification of the mutant allele with an oligonucleotide primer consisting of the sequence set forth as SEQ ID NO: 3, as disclosed in the examples of the instant specification (p.31 ln.22; Table 3). Thus the asserted unexpected result taught by the instant specification is not commensurate in scope with the breadth of the claims. While the claims broadly encompass the use of a multitude of primers with a wide variety of nucleotide sequences, the specification in fact only teaches the use of a mutant-allele-specific primer consisting of SEQ ID NO: 3.

The claims have been amended to recite ‘wherein the 3’-end nucleotide of said nucleotide sequence is cytidine’, and applicants argue that this amendment more distinctly points out that in their claimed methods ‘the 3’-end nucleotide or 3’ terminus of the mutant-allele-specific primer is cytidine’. This is not found to be persuasive. If applicant intends for the claim to be limited to a primer in which the 3’-terminal nucleotide is a cytidine, and the particular cytidine is in a mismatch with particular template nucleotide, the claim should be written as such or be amended to require a mutant-allele-specific primer consisting of a particular SEQ ID NO.

Applicants argue that DelRio-LaFreniere et al does not provide particular motivation to create a mutant-allele-specific primer with a cytidine as the 3'-end nucleotide that is capable of annealing to the complement of nucleotides 3 to 23 of SEQ ID NO: 12, and that DelRio-LaFreniere et al teaches that testing is required to establish optimal allele specific primers that incorporate intentional mismatches (arguments page 17). This argument is not found to be persuasive because, as noted above, the claims do not in fact require a mutant-allele-specific primer consisting of a specific nucleotide sequence and having with an intentionally mismatched cytidine residue as the 3'-terminal nucleotide. Given the breadth of the claims as written, the teachings of DelRio-LaFreniere et al regarding intentional mismatches in allele specific primers would lead one of ordinary skill in the art to create primers that satisfy the limitations of the broadly claimed primers of the instant application.

The rejection is MAINTAINED.

Applicants have traversed the rejection of claims 2, 4, 5, 16, 18, 19, and 30 as obvious over Hucl et al in view of DelRio-LaFreniere et al and further in view of Stanton, and the rejection of claims 3, 17, and 31 as obvious over Hucl et al in view of DelRio-LaFreniere et al and Stanton and further in view of Werle et al. As detailed above, Applicants argue that the unexpected results regarding mutant-allele-specific primers taught by the instant specification are not obvious in view of the teachings of DelRio-LaFreniere et al, and that the amended claims more distinctly point out that the 3'-end nucleotide of the mutant-allele-specific primer is cytidine. As detailed above,

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considering the breadth of the claims as written (e.g. a lack of a clearly defined nucleotide sequence of the mutant-allele-specific primer), the asserted unexpected result is not commensurate in scope with the breadth of the claims, and the claims do not particularly require a primer with a mismatched cytidine at the 3'-terminus that is particularly mismatched with the nucleotide variation of interest.

The rejections are MAINTAINED.

Applicant's amendment necessitated any new ground(s) of rejection presented in this Office action. Accordingly, THIS ACTION IS MADE FINAL. See MPEP § 706.07(a). Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the date of this final action.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Stephen Kapushoc whose telephone number is 571-272-3312. The examiner can normally be reached on Monday through Friday, from 8am until 5pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Ram Shukla can be reached at 571-272-0735. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Stephen Kapushoc
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CARLA J. MYERS
PRIMARY EXAMINER